

Differential responses to kinase inhibition in FGFR2-addicted triple negative breast cancer cells: a quantitative phosphoproteomics study

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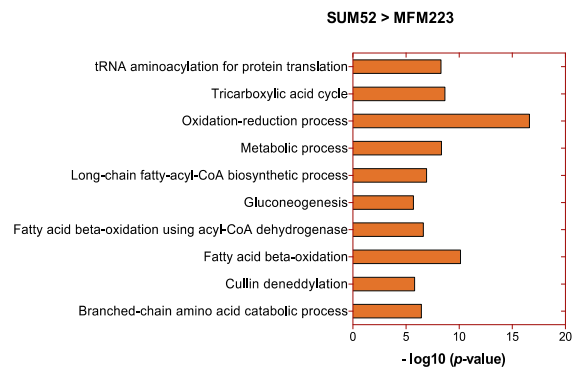
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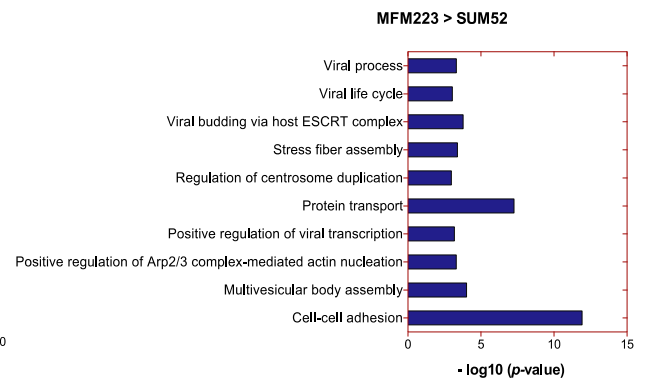
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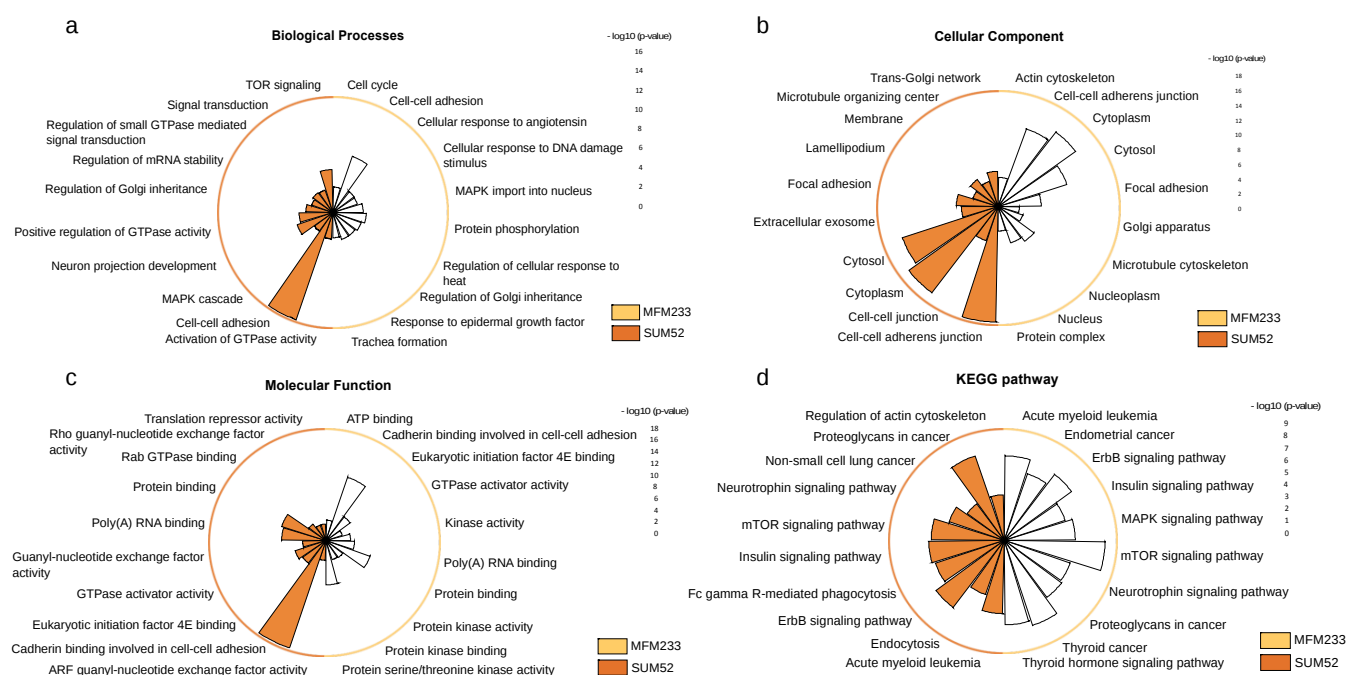
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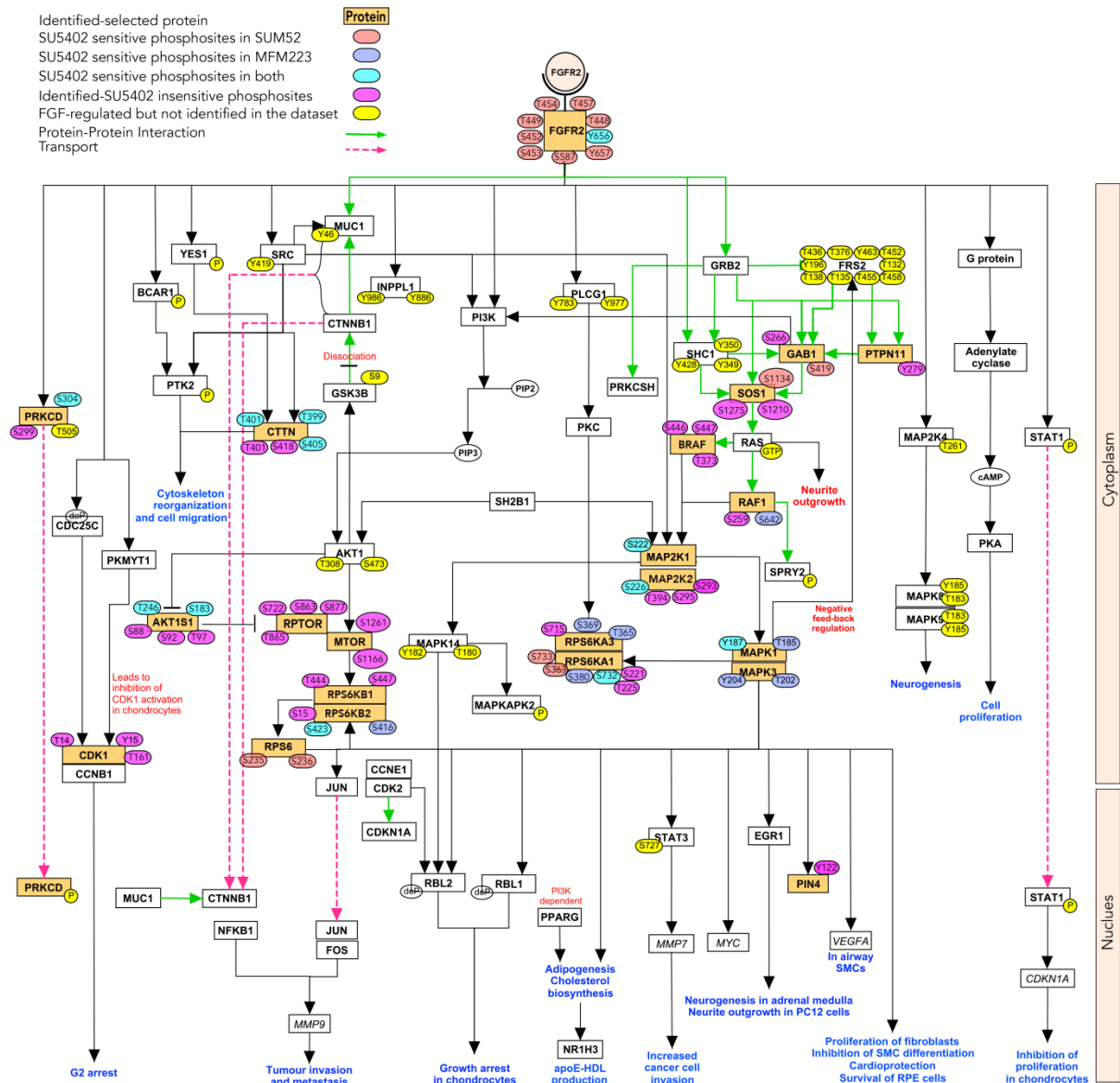
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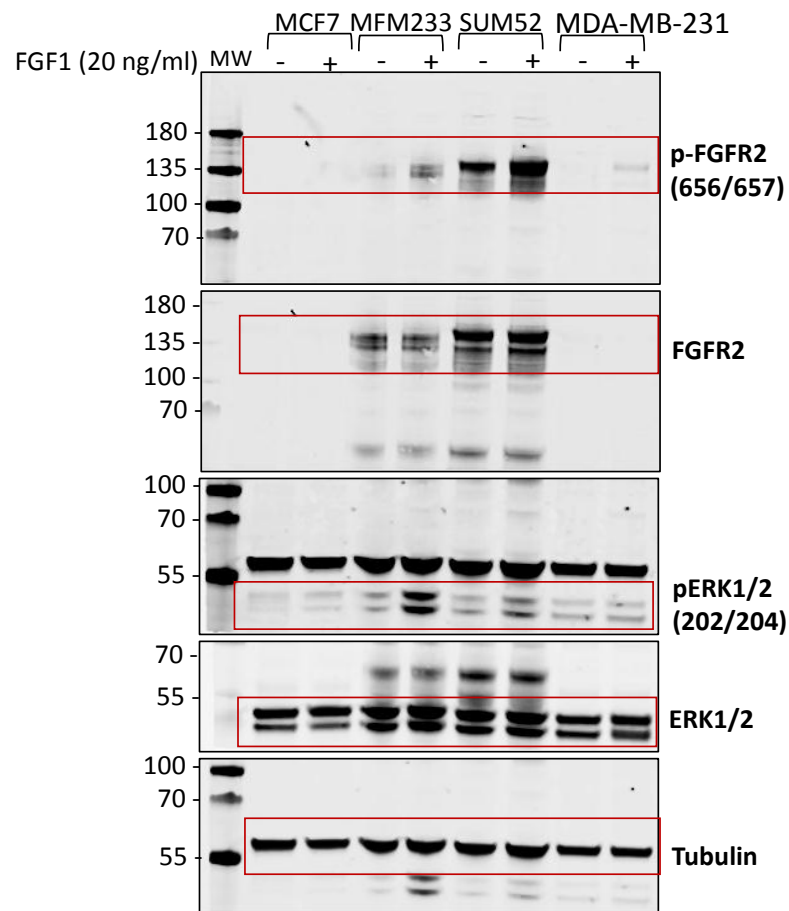
Supplementary Figure S1. Differentially expressed proteins were analysed in DAVID¹ to identify enriched GO Biological Processes. The top 10 enriched categories for proteins with a high SUM52/MFM223 ratio (a) or a low SUM52/MFM223 ratio (b) are plotted as bar charts.



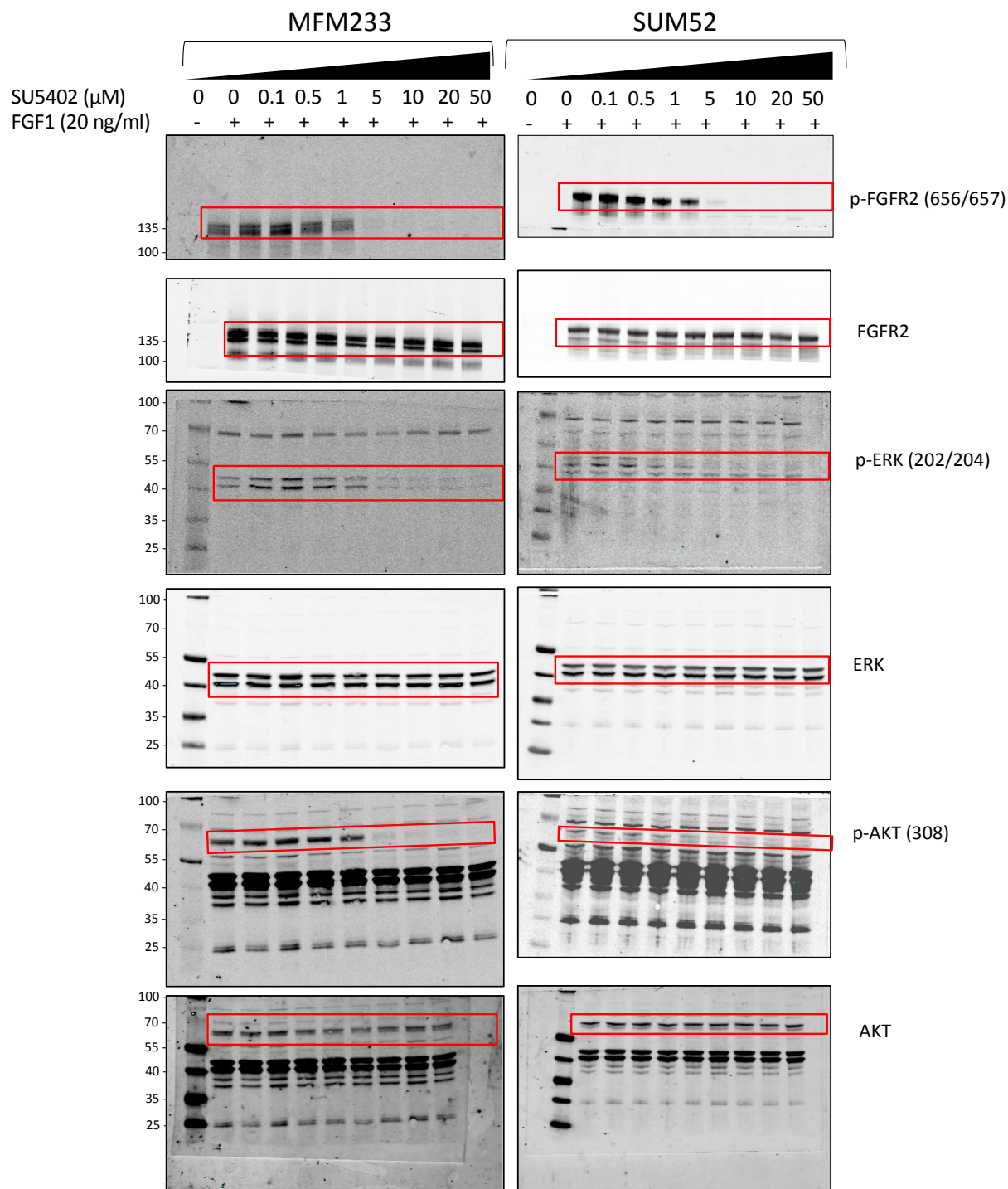
Supplementary Figure S2. GO-term analysis of differentially SU5402-sensitive phosphopeptides in SUM52 and MFM223 cells. Proteins which contained SU5402-sensitive phosphopeptides in either SUM52 or MFM223 cells were analysed in DAVID¹ to identify enriched GO Biological Processes (a), Cellular Components (b), Molecular Functions (c) or KEGG pathways (d). The top 10 enriched categories are plotted within a radar chart.



Supplementary Figure S3. A detailed map of FGFR2 signalling created by NetPath². SU5402 sensitive and insensitive phosphosites found within MFM223 and SUM52 dataset visualised within the FGF signalling network.



Supplementary Figure S4. MCF7, MFM223, and SUM52 cells were stimulated with 20 ng/mL FGF1 for 30 min. Levels of p-FGFR2 (pY656pY657), FGFR2, and tubulin in unstimulated and FGF1-stimulated whole cell lysates were analysed by western blotting. Boxes indicate cropped regions displayed in Figure 1c.



Supplementary Figure S5. MFM233 and SUM52 cells were stimulated with 20 ng/mL FGF1 for 30 min in the presence of increasing concentrations of SU5402. Levels of p-FGFR2 (pY656pY657), FGFR2, p-ERK (T202Y204), ERK, p-AKT (T308), and AKT in whole cell lysates were analysed by western blotting. Boxes indicate cropped regions displayed in Figure 2b.

Supplementary References

1. Huang, D. W., Sherman, B. T. & Lempicki, R. A. Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. *Nat. Protoc.* **4**, 44–57 (2009).
2. Raju, R. et al. NetSlim: high-confidence curated signaling maps. *Database* 2011:bar032. (2011).